# FIGURE 1

```
   1 ATG AAC TTC CTT AAG TCT TTC CCT TTC TAC GCT TTC CTT TGT TTC GGT CAA TAC TTC GTT   60
   1 M   N   F   L   K   S   F   P   F   Y   A   F   L   C   F   G   Q   Y   F   V    20

  60 GCT GTT ACT CAC GCT GCT GAG ATC ACC CGC ATT CCT CTC TAC AAA GGT AAG TCT CTC CGT  120
  21 A   V   T   H   A   A   E   I   T   R   I   P   L   Y   K   G   K   S   L   R    40

 121 AAG GCG CTG AAG GAA CAT GGA CTT CTA GAA GAC TTC TTG CAG AAA CAA CAG TAT GGC ATC  180
  41 K   A   L   K   E   H   G   L   L   E   D   F   L   Q   K   Q   Q   Y   G   I    60

 181 AGC AGC AAG TAC TCC GGC TTC GGT GAA GTT GCT AGC GTG CCA CTT ACC AAC TAC CTT GAT  240
  61 S   S   K   Y   S   G   F   G   E   V   A   S   V   P   L   T   N   Y   L   D    80

 241 AGT CAA TAC TTT GGG AAG ATC TAC CTC GGA ACC CCG CCT CAA GAG TTC ACC GTT CTC TTT  300
  81 S   Q   Y   F   G   K   I   Y   L   G   T   P   P   Q   E   F   T   V   L   F   100

 301 GAT ACT GGT TCC TCT GAC TTC TGG GTT CCC TCT ATC TAC TGC AAG AGC AAT GCC TGC AAG  360
 101 D   T   G   S   S   D   F   W   V   P   S   I   Y   C   K   S   N   A   C   K   120

 361 AAC CAC CAA AGA TTC GAT CCG AGA AAG TCG TCC ACC TTC CAG AAC TTA GGC AAA CCC TTG  420
 121 N   H   Q   R   F   D   P   R   K   S   S   T   F   Q   N   L   G   K   P   L   140

 420 TCT ATA CAC TAC GGT ACA GGT AGC ATG CAA GGA ATC TTA GGC TAT GAT ACC GTC ACT GTC  480
 141 S   I   H   Y   G   T   G   S   M   Q   G   I   L   G   Y   D   T   V   T   V   160

 481 TCC AAC ATT GTG GAC ATT CAA CAG ACA GTA GGA CTT AGC ACC CAA GAA CCA GGT GAT GTC  540
 161 S   N   I   V   D   I   Q   Q   T   V   G   L   S   T   Q   E   P   G   D   V   180

 541 TTC ACC TAT GCA GAA TTC GAT GGC ATC CTT GGT ATG GCA TAC CCA TCG CTC GCG TCA GAG  600
 181 F   T   Y   A   E   F   D   G   I   L   G   M   A   Y   P   S   L   A   S   E   200

 601 TAC TCG ATA CCT GTG TTT GAC AAC ATG ATG AAC CGA CAC CTA GTA GCT CAA GAC TTG TTC  660
 201 Y   S   I   P   V   F   D   N   M   M   N   R   H   L   V   A   Q   D   L   F   220

 661 TCG GTT TAC ATG GAC AGG AAT GGC CAG GAG AGC ATG CTC ACG CTT GGA GCT ATT GAT CCA  720
 221 S   V   Y   M   D   R   N   G   Q   E   S   M   L   T   L   G   A   I   D   P   240

 721 TCC TAC TAC ACA GGA TCT CTT CAC TGG GTT CCA GTC ACT GTG CAG CAG TAC TGG CAA TTC  780
 241 S   Y   Y   T   G   S   L   H   W   V   P   V   T   V   Q   Q   Y   W   Q   F   260

 781 ACT GTG GAC AGT GTC ACC ATC AGC GGT GTG GTT GTT GCA TGT GAA GGT GGA TGT CAA GCT  840
 261 T   V   D   S   V   T   I   S   G   V   V   V   A   C   E   G   G   C   Q   A   280

 841 ATC TTG GAT ACC GGT ACG TCC AAG CTG GTC GGA CCT AGC AGC GAC ATT CTC AAC ATT CAG  900
 281 I   L   D   T   G   T   S   K   L   V   G   P   S   S   D   I   L   N   I   Q   300

 901 CAA GCT ATT GGA GCC ACA CAG AAC CAG TAC GGT GAG TTT GAC ATA GAT TGC GAC AAC CTT  960
 301 Q   A   I   G   A   T   Q   N   Q   Y   G   E   F   D   I   D   C   D   N   L   320

 961 AGC TAC ATG CCT ACA GTT GTC TTT GAG ATC AAC GGC AAG ATG TAC CCA CTG ACC CCC TCC 1020
```

# FIGURE 1 cont'd

```
321 S   Y   M   P   T   V   V   F   E   I   N   G   K   M   Y   P   L   T   P   S    340
1021 GCC TAT ACC AGC CAG GAT CAA GGG TTC TGC ACC AGT GGA TTC CAG AGT GAG AAC CAT TCC 1080
 341 A   Y   T   S   Q   D   Q   G   F   C   T   S   G   F   Q   S   E   N   H   S    360

1081 CAG AAA TGG ATC TTG GGA GAT GTG TTC ATT CGT GAG TAC TAC AGC GTC TTT GAC AGG GCC 1140
 361 Q   K   W   I   L   G   D   V   F   I   R   E   Y   Y   S   V   F   D   R   A    380

1141 AAC AAC CTC GTT GGG CTA GCT AAA GCA ATC TGA  1200
 381 N   N   L   V   G   L   A   K   A   I   *    391
```

# FIGURE 2

```
   1 ctgcaggaattcattgtactcccagtatcattatagtgaaagttttggctctctcgccggtggtttttttacctctattta  80

  81 aaggggttttccacctaaaaattctggtatcattctcactttacttgttactttaatttctcataatctttggttgaaat 160

 161 tatcacgcttccgcacacgatatccctacaaatttattatttgttaaacattttcaaaccgcataaaattttatgaagtc 240

 241 ccgtctatctttaatgtagtctaacattttcatattgaaatatataatttacttaattttagcgttggtagaaagcataa 320

 321 agatttattcttattcttcttcatataaatgtttaatatacaatataaacaaattctttaccttaagaaggatttcccat 400

 401 tttatattttaaaaatatatttatcaaatatttttcaaccacgtaaatctcataataataagttgtttcaaaagtaataa 480

 481 aatttaactccataatttttttattcgactgatcttaaagcaacacccagtgacacaactagccatttttttctttgaat 560

 561 aaaaaaatccaattatcattgtatttttttttatacaatgaaaatttcaccaaacaatcatttgtggtatttctgaagcaa 640

 641 gtcatgttatgcaaaattctataattcccatttgacactacggaagtaactgaagatctgcttttacatgcgagacacat 720

 721 cttctaaagtaattttaataatagttactatattcaagatttcatatatcaaatactcaatattacttctaaaaaattaa 800

 801 ttagatataattaaaatattacttttttaattttaagtttaattgttgaatttgtgactattgatttattattctactat 880

 881 gtttaaattgttttatagatagtttaaagtaaatataagtaatgtagtagagtgttagagtgttaccctaaaccataaac 960

 961 tataacatttatggtggactaattttcatatatttcttattgcttttacctttttcttggtatgtaagtccgtaactagaa 1040

1041 ttacagtgggttgccatggcactctgtggtcttttggttcatgcatgggtcttgcgcaagaaaaagacaaagaacaaaga 1120

1121 aaaaagacaaaacagagagacaaaacgcaatcacacaaccaactcaaattagtcactggctgatcaagatcgccgcgtcc 1200

1201 atgtatgtctaaatgccatgcaaagcaacacgtgcttaacatgcactttaaatggctcacccatctcaacccacacacaa 1280

1281 acacattgccttttttcttcatcatcaccacaaccacctgtatatattcattctcttccgccacctcaatttcttcacttc 1360

1361 aacacacgtcaacctgcatatgcgtgtcatcccatgcccaaatctccatgcatgttccaaccaccttctctcttatataa 1440

1441 tacctataaatacctctaatatcactcacttctttcatcatccatccatccagagtactactactctactactataatac 1520

1521 cccaacccaactcatattcaatactactctact ATG AAC TTC CTT AAG TCT TTC CCT TTC TAC GCT    1586
   1                                  M   N   F   L   K   S   F   P   F   Y   A      11

1587 TTC CTT TGT TTC GGT CAA TAC TTC GTT GCT GTT ACT CAC GCT GCT GAG ATC ACC CGC ATT  1646
  12 F   L   C   F   G   Q   Y   F   V   A   V   T   H   A   A   E   I   T   R   I   31

1647 CCT CTC TAC AAA GGT AAG TCT CTC CGT AAG GCG CTG AAG GAA CAT GGA CTT CTA GAA GAC  1706
  32 P   L   Y   K   G   K   S   L   R   K   A   L   K   E   H   G   L   L   E   D   51

1707 TTC TTG CAG AAA CAA CAG TAT GGC ATC AGC AGC AAG TAC TCC GGC TTC GGT GAA GTT GCT  1766
  52 F   L   Q   K   Q   Q   Y   G   I   S   S   K   Y   S   G   F   G   E   V   A   71

1767 AGC GTG CCA CTT ACC AAC TAC CTT GAT AGT CAA TAC TTT GGG AAG ATC TAC CTC GGA ACC  1826
  72 S   V   P   L   T   N   Y   L   D   S   Q   Y   F   G   K   I   Y   L   G   T   91
```

# FIGURE 2 cont'd

```
1827 CCG CCT CAA GAG TTC ACC GTT CTC TTT GAT ACT GGT TCC TCT GAC TTC TGG GTT CCC TCT 1886
  92 P   P   Q   E   F   T   V   L   F   D   T   G   S   S   D   F   W   V   P   S   111

1887 ATC TAC TGC AAG AGC AAT GCC TGC AAG AAC CAC CAA AGA TTC GAT CCG AGA AAG TCG TCC 1946
 112 I   Y   C   K   S   N   A   C   K   N   H   Q   R   F   D   P   R   K   S   S   131

1947 ACC TTC CAG AAC TTA GGC AAA CCC TTG TCT ATA CAC TAC GGT ACA GGT AGC ATG CAA GGA 2006
 132 T   F   Q   N   L   G   K   P   L   S   I   H   Y   G   T   G   S   M   Q   G   151

2007 ATC TTA GGC TAT GAT ACC GTC ACT GTC TCC AAC ATT GTG GAC ATT CAA CAG ACA GTA GGA 2066
 152 I   L   G   Y   D   T   V   T   V   S   N   I   V   D   I   Q   Q   T   V   G   171

2067 CTT AGC ACC CAA GAA CCA GGT GAT GTC TTC ACC TAT GCA GAA TTC GAT GGC ATC CTT GGT 2126
 172 L   S   T   Q   E   P   G   D   V   F   T   Y   A   E   F   D   G   I   L   G   191

2127 ATG GCA TAC CCA TCG CTC GCG TCA GAG TAC TCG ATA CCT GTG TTT GAC AAC ATG ATG AAC 2186
 192 M   A   Y   P   S   L   A   S   E   Y   S   I   P   V   F   D   N   M   M   N   211

2187 CGA CAC CTA GTA GCT CAA GAC TTG TTC TCG GTT TAC ATG GAC AGG AAT GGC CAG GAG AGC 2246
 212 R   H   L   V   A   Q   D   L   F   S   V   Y   M   D   R   N   G   Q   E   S   231

2247 ATG CTC ACG CTT GGA GCT ATT GAT CCA TCC TAC TAC ACA GGA TCT CTT CAC TGG GTT CCA 2306
 232 M   L   T   L   G   A   I   D   P   S   Y   Y   T   G   S   L   H   W   V   P   251

2307 GTC ACT GTG CAG CAG TAC TGG CAA TTC ACT GTG GAC AGT GTC ACC ATC AGC GGT GTG GTT 2366
 252 V   T   V   Q   Q   Y   W   Q   F   T   V   D   S   V   T   I   S   G   V   V   271

2367 GTT GCA TGT GAA GGT GGA TGT CAA GCT ATC TTG GAT ACC GGT ACG TCC AAG CTG GTC GGA 2426
 272 V   A   C   E   G   G   C   Q   A   I   L   D   T   G   T   S   K   L   V   G   291

2427 CCT AGC AGC GAC ATT CTC AAC ATT CAG CAA GCT ATT GGA GCC ACA CAG AAC CAG TAC GGT 2486
 292 P   S   S   D   I   L   N   I   Q   Q   A   I   G   A   T   Q   N   Q   Y   G   311

2487 GAG TTT GAC ATA GAT TGC GAC AAC CTT AGC TAC ATG CCT ACA GTT GTC TTT GAG ATC AAC 2546
 312 E   F   D   I   D   C   D   N   L   S   Y   M   P   T   V   V   F   E   I   N   331

2547 GGC AAG ATG TAC CCA CTG ACC CCC TCC GCC TAT ACC AGC CAG GAT CAA GGG TTC TGC ACC 2606
 332 G   K   M   Y   P   L   T   P   S   A   Y   T   S   Q   D   Q   G   F   C   T   351

2607 AGT GGA TTC CAG AGT GAG AAC CAT TCC CAG AAA TGG ATC TTG GGA GAT GTG TTC ATT CGT 2666
 352 S   G   F   Q   S   E   N   H   S   Q   K   W   I   L   G   D   V   F   I   R   371

2667 GAG TAC TAC AGC GTC TTT GAC AGG GCC AAC AAC CTC GTT GGG CTA GCT AAA GCA ATC TGA 2726
 372 E   Y   Y   S   V   F   D   R   A   N   N   L   V   G   L   A   K   A   I   *   391

2727 agcttaataagtatgaactaaaatgcatgtaggtgtaagagctcatggagagcatggaatattgtatccgaccatgtaac 2806

2807 agtataataactgagctccatctcacttcttctatgaataaacaaaggatgttatgatatattaacactctatctatgca 2886

2887 ccttattgttctatgataaatttcctcttattattataaatcatctgaatcgtgacggcttatggaatgcttcaaatagt 2966
```

# FIGURE 2 cont'd

2967 acaaaaacaaatgtgtactataagactttctaaacaattctaactttagcattgtgaacgagacataagtgttaagaaga 3046

3047 cataacaattataatggaagaagtttgtctccatttatatattatatattacccacttatgtattatattaggatgttaa 3126

3127 ggagacataacaattataaagagagaagtttgtatccatttatatattatatactacccatttatatattatacttatcc 3206

3207 acttatttaatgtctttataaggtttgatccatgatatttctaatattttagttgatatgtatatgaaagggtactattt 3286

3287 gaactctcttactctgtataaaggttggatcatccttaaagtgggtctatttaattttattgcttcttacagataaaaaa 3366

3367 aaaattatgagttggtttgataaaatattgaaggatttaaaataataataaataataaataacatataatatatgtatat 3446

3447 aaatttattataatataacatttatctataaaaaagtaaatattgtcataaatctatacaatcgtttagccttgctggac 3526

3527 gactctcaattatttaaacgagagtaaacatatttgacttttggttatttaacaaattattatttaacactatatgaaa 3606

3607 tttttttttttatcggcaaggaaataaaattaaattaggagggacaatggtgtgtcccaatccttatacaaccaacttc 3686

3687 cacaggaaggtcaggtcggggacaacaaaaaaacaggcaagggaaatttttttaatttgggttgtcttgtttgctgcataa 3766

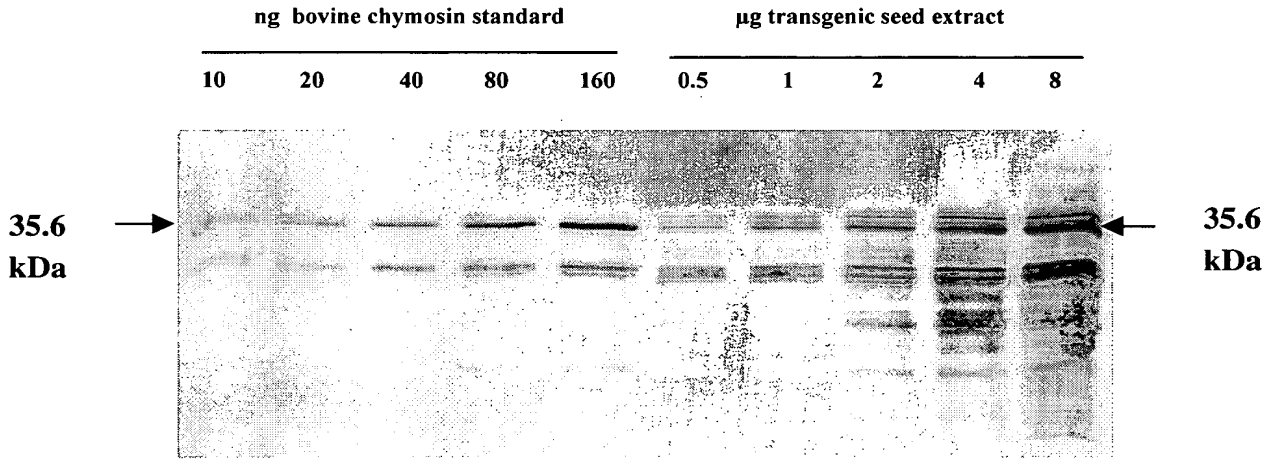
3767 tttatgcagtaaaacactacacataacccttttagcagtagagcaatggttgaccgtgtgcttagcttctttttatttttat 3846

3847 ttttttatcagcaaagaataaataaaataaaatgagacacttcagggatgtttcaacccttatacaaaaccccaaaaaca 3926

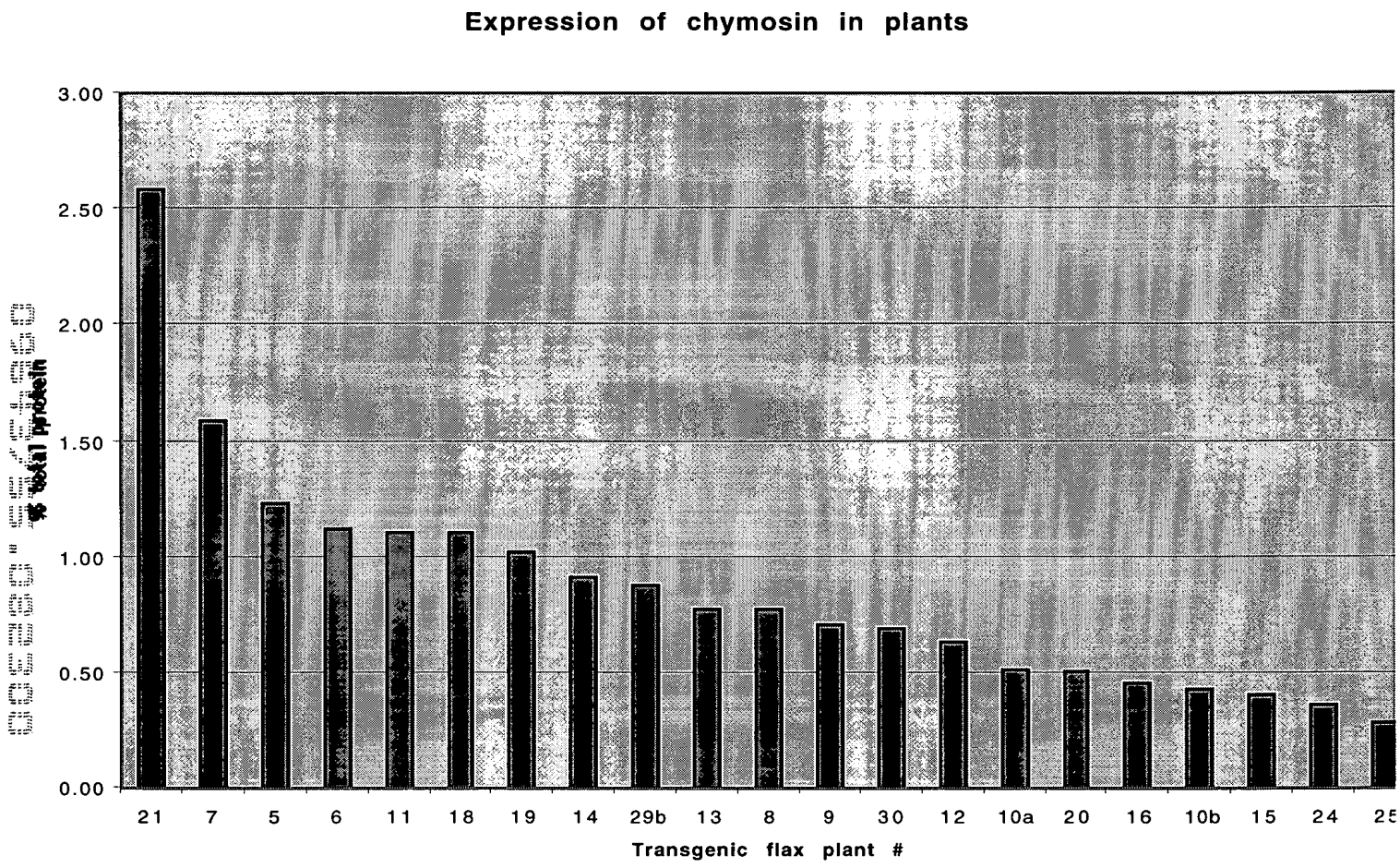
3927 agtttcctagcaccctaccaactaaggtacc 3957

Substitute Sheet (Rule 26)

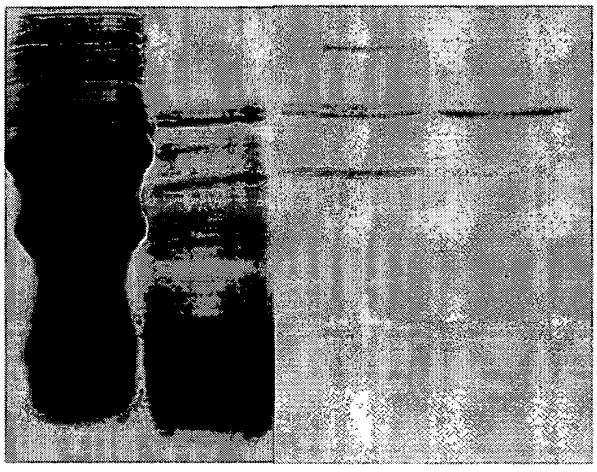
# FIGURE 3


ng bovine chymosin standard
µg transgenic seed extract
10
20
40
80
160
0.5
1
2
4
8
35.6
kDa
35.6
kDa

# FIGURE 4


Expression of chymosin in plants
% total protein
3.00
2.50
2.00
1.50
1.00
0.50
0.00
21
7
5
6
11
18
19
14
29b
13
8
9
30
12
10a
20
16
10b
15
24
25
Transgenic flax plant #

# FIGURE 5



Mature
chymosin
(35.6 kDa)

1 2 3 4